

### AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning on page 3, line 16, to read as follows:

Fig. 2 shows the multiple alignment of amino acid sequences of IPMDH and ICDH from various biological species (see also Table 1). The partial amino acid sequences in Fig. 2 are shown as sequence SEQ ID:1 to SEQ ID:48 in order in the sequence listing.

Please amend the paragraph beginning on page 3, line 26, to read as follows:

Fig. 6 shows the nucleotide sequence (nucleotides 1-576 of SEQ ID: 49, top strand) and amino acid sequence (amino acid residues 1-192 of SEQ ID: 50, bottom strand) of *Sulfolobus* sp. *leuB* gene.

Please amend the paragraph beginning on page 3, line 28, to read as follows:

Fig. 7 shows the nucleotide sequence (nucleotides 577-1014 of SEQ ID: 49, top strand) and amino acid sequence (amino acid residues 193-337 of SEQ ID: 50, bottom strand) of *Sulfolobus* sp. *leuB* gene (continuation of Fig. 6).

Please amend the paragraph beginning on page 4, line 4, to read as follows:

Fig. 9 shows the multiple alignment of amino acid sequences of IPMDH and ICDH. The sequences with (ICDH) represent ICDH sequence and the sequences without the indication represent the IPMDH sequence. N. Cra: *Neurospora crassa* (SEQ IDs: 57-59), S. Cer: *Saccharomyces cerevisiae* (SEQ IDs: 60-62), A. tum: *Agrobacterium tumefaciens* (SEQ IDs: 63-65), B. sub: *Bacillus subtilis* (SEQ IDs: 66-68), E. Col: *Escherichia coli* (SEQ IDs: 69-71), T. The: *Thermus thermophilus* (SEQ IDs: 72-74), Sub sp.#7: *Sulfolobus* stain #7 (SEQ IDs: 75-77), Cs. Cer: *Saccharomyces cerevisiae* (ICDH) (SEQ IDs: 78-80), CB. Tau: *Bos taurus*(ICDH) (SEQ IDs: 81-83), CB. Sub: *Bacillus subtilis*(ICDH) (SEQ IDs: 84-86), CE. Col: *Escherichia coli* (ICDH) (SEQ IDs: 87-89).

Please amend the paragraph beginning on page 4, line 17, to read as follows:

Fig. 13 shows the multiple alignment of IPMDH and ICDH. The partial amino acid sequences in Fig. 13 are shown as sequence SEQ ID:95 to SEQ ID:104 in order in the sequence listing.

Please amend the paragraph beginning on page 17, Table 1, to read as follows:

Table 1

Multiple alignment of amino acid sequences of IPMDH and ICDH

Enzyme and species	Partial amino acid sequence						
IPMDH	89	97	150	158	256	263	280 285
<i>Sulfolobus</i> sp. <del>strain</del> □ <u>strain 7</u>	YDMYANIRP---	I	AKVG	LNFA---	VHGA	AFDI---	MMYERM
<i>Thermus thermophilus</i>	QDLFANLRP---	V	ARVA	FEAA---	VHGS	APDI---	MMLEHA
<i>Bacillus subtilis</i>	LDLFANLRP---	V	IREG	FKMA---	VHGS	APDI---	MLLRYS
<i>Escherichia coli</i>	FKLFNSLRP---	I	ARIA	FESA---	AGGS	APDI---	LLLRYS
<i>Agrobacterium tumefaciens</i>	LELFANLRP---	I	ASVA	FELA---	VHGS	APDI---	MCLRYS
<i>Saccharomyces cerevisiae</i>	LQLYANLRP---	I	TRMA	AFMA---	CHGS	APDL---	MMLKLS
<i>Neurospora crassa</i>	LGTYGNLRP---	I	ARLAG	FLA---	IHGS	APDI---	MMLRYS
ICDH	89	97	150	158	256	263	280 285
<i>Saccharomyces cerevisiae</i>	FGLFANVRP---	V	IRYA	FEYA---	VHGS	APDI---	MMLNHM
<i>Bos Taurus</i> (3/4)	FDLYANVRP---	I	AEFA	FEYA---	VHGT	APDI---	MMLRHM
<i>Bacillus subtilis</i>	LDL FVCLRP---	L	VRAA	IDYA---	THGT	APKY---	LLLEHL
<i>Escherichia coli</i>	LDLYICLRP---	L	VRAA	IEYA---	THGT	APKY---	MMLRHM
Ancestral species (predicted)	xDLxANLRP---	I	ARxA	FExA---	VHGS	APDI---	MMLxxx
modified amino acids and their positions	L	L	R	A	S	P	L
	<a region>	<b region>	<c region>	<d region>			
		b'	b''				